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RAW SEQUENCE LISTING PATENT APPLICATION US/08/905,293

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This Raw Listing contains the General Information Section and up to the first 5 pages.

1		General Information (i) APPLICANT: Yelton, Dale E.
2		
3	(1)	General Information
4		
5		(i) APPLICANT: Yelton, Dale E.
6		Rosok, Mae Joanne
7		
8		(ii) TITLE OF THE INVENTION: A METHOD FOR INHIBITING IMMUNOGLOBULIN-
9		
10		(iii) NUMBER OF SEQUENCES: 27
11		
12		(iv) CORRESPONDENCE ADDRESS:
13		(A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
14		(B) STREET: 11150 Santa Monica Boulevard, Suite 400
15		(C) CITY: Los Angeles
16		(D) STATE: CA
17		(E) COUNTRY: USA
18		(F) ZIP: 90025
19		
20		(V) COMPUTER READABLE FORM:
21		(A) MEDIUM TYPE: Diskette
22		(B) COMPUTER: IBM Compatible
23		(C) OPERATING SYSTEM: DOS
24		(D) SOFTWARE: FastSEQ for Windows Version 2.0
25		
26		(vi) CURRENT APPLICATION DATA:
27		(A) APPLICATION NUMBER: 08/905,293
28		(B) FILING DATE: 01-AUG-1997
29		(C) CLASSIFICATION:
30		
31		(vii) PRIOR APPLICATION DATA:
32		(A) APPLICATION NUMBER: 60/023,033
33		(B) FILING DATE: 02-AUG-1996
34		
35		
36		
37		(viii) ATTORNEY/AGENT INFORMATION:
38		(A) NAME: Canady, Karen S
39		(B) REGISTRATION NUMBER: 39,927
40		(C) REFERENCE/DOCKET NUMBER: 30436.43USU1
41		
42		(ix) TELECOMMUNICATION INFORMATION:
43		(A) TELEPHONE: 310-445-1140
44		(B) TELEFAX: 310-445-9031
45		(C) TELEX:

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47		
48	(2) INFORMATION FOR SEQ ID NO:1:	
49		
50	(i) SEQUENCE CHARACTERISTICS:	
51	(A) LENGTH: 36 base pairs	
52	(B) TYPE: nucleic acid	
53	(C) STRANDEDNESS: single	
54	(D) TOPOLOGY: linear	
55		
56	(ii) MOLECULE TYPE: cDNA	
57		
58	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
59		26
60	TGGCACCGAA AGCTTTCTGG GGCAGGCCAG GCCTGA	36
61		
62	(2) INFORMATION FOR SEQ ID NO:2:	
63	A LA GRANDA GUARA	
64	(i) SEQUENCE CHARACTERISTICS:	
65	(A) LENGTH: 57 base pairs	
66	(B) TYPE: nucleic acid	
67	(C) STRANDEDNESS: single	
68	(D) TOPOLOGY: linear	
69	(11) VOLEGUE BUNDE - PNA	
70	(ii) MOLECULE TYPE: cDNA	
71	(- 1) GROUPINGE PROGRESSION, GRO TO NO. O.	
72	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
73 74	TCCGGACATG TTGGTACCCA CGTGGTGGTC GACGCTGAGC CTGGCTTCGA GCAGACA	57
7 4 75	TECGGACATG TIGGTACCCA EGIGGIGGIC GACGETGAGE ETGGETTEGA GEAGACA	37
76	(2) INFORMATION FOR SEQ ID NO:3:	
77	(2) INFORMATION FOR SEQ ID NO.3.	
78	(i) SEQUENCE CHARACTERISTICS:	
79	(A) LENGTH: 55 base pairs	
80	(B) TYPE: nucleic acid	
81	(C) STRANDEDNESS: single	
82	(D) TOPOLOGY: linear	
83	(b) 10100011 1111001	
84	(ii) MOLECULE TYPE: cDNA	
85	(,	
86	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
87	(······/ ······························	
88	GTCGACCACC ACGTGGGTAC CAACATGTCC GGAGCCACAT GGACAGAGGC CGGCT	55
89		
90	(2) INFORMATION FOR SEQ ID NO:4:	
91		
92	(i) SEQUENCE CHARACTERISTICS:	
93	(A) LENGTH: 30 base pairs	
94	(B) TYPE: nucleic acid	
95	(C) STRANDEDNESS: single	
96	(D) TOPOLOGY: linear	
97		
98	(ii) MOLECULE TYPE: cDNA	

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100	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
101		
102	CTGGTTCTTG GTCATCTCCT CTCTAGATGG	30
103		
104	(2) INFORMATION FOR SEQ ID NO:5:	
105		
106	(i) SEQUENCE CHARACTERISTICS:	
107	(A) LENGTH: 36 base pairs	
108	(B) TYPE: nucleic acid	
109	(C) STRANDEDNESS: single	
110	(D) TOPOLOGY: linear	
111		
112	(ii) MOLECULE TYPE: cDNA	
113		
114	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
115		
116	ACCATGGTCG ACCTCAGACC TGCCAAGAGC CATATC	36
117		
118	(2) INFORMATION FOR SEQ ID NO:6:	
119		
120	(i) SEQUENCE CHARACTERISTICS:	
121	(A) LENGTH: 40 base pairs	
122	(B) TYPE: nucleic acid	
123	(C) STRANDEDNESS: single	
124	(D) TOPOLOGY: linear	
125		
126	(ii) MOLECULE TYPE: cDNA	
127	()	
128	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
129	·	
130	CATGGTCACG TGGTGTGTCC CTGGATGCAG GCTACTCTAG	40
131		
132	(2) INFORMATION FOR SEQ ID NO:7:	
133	(-)	
134	(i) SEQUENCE CHARACTERISTICS:	
135	(A) LENGTH: 49 base pairs	
136	(B) TYPE: nucleic acid	
137	(C) STRANDEDNESS: single	
138	(D) TOPOLOGY: linear	
139		
140	(ii) MOLECULE TYPE: cDNA	
141	(,	
142	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
143	(nz) bagaana babanzi izan bag ib navi	
144	CAGGGAGGGA GGGTGTCTGC TGGAAGCCAG GCTCAGCGCT GACCTCAGA	49
145	0,,000,000,,000,,000,,000,,000,,000,,000,,000,,000,,000,,000,,000,,000,000,,0000	
146	(2) INFORMATION FOR SEQ ID NO:8:	
147	10) THE COMMITTON TON DAY TO MOTO.	
148	(i) SEQUENCE CHARACTERISTICS:	
149	(A) LENGTH: 50 base pairs	
150	(B) TYPE: nucleic acid	
151	(C) STRANDEDNESS: single	
152	(D) TOPOLOGY: linear	
	(5) 1010201. 1111001	

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153 154	(11)	MOLECULE T	ADE. CUMP				
155	(11)	MODECOLE 1.	IFE. CDNA				
156	(vi)	SEQUENCE DI	· WOTTOTADE	SEO TO NO.	R •		
157	(* +)	SEQUENCE D	BORIL IION.	DDQ ID NO.			
158	GGAAAGAACC	ATCACAGTCT	CGCAGGGGCC	CAGGGCAGCG	CTGGGTGCTT		50
159							
160	()	2) INFORMAT	ON FOR SEQ	ID NO:9:			
161	,	•	_				
162	(i) :	SEQUENCE CHA	ARACTERISTIC	CS:			
163) LENGTH: 8		irs			
164	(B)) TYPE: nucl	leic acid				
165	(C)) STRANDEDNI	ESS: single		•		
166	(D)	TOPOLOGY:	linear				
167							
168	(ii)	MOLECULE T	YPE: cDNA				
169							
170	(xi)	SEQUENCE DE	ESCRIPTION:	SEQ ID NO:	9:		
171							
172						GCCAGAGTAA	60
: 173		TAATTTTATT	+				120
174		GTCGACTCTC					180
175		TTGTGTGTTG					240
176		CTTGACCGAC					300
177	•	TGTACGGGCC					360
178		TACGGGGTCA					420
179						ACGTCAATAA	480
180		TCCCATAGTA					540
181		AACTGCCCAC					600
182		CAATGACGGT					660
183		TACTTGGCAG					720
184		GTACATCAAT					780
185		TGACGTCAAT					840
186		CAACTCCGCC					900 960
187		TCACTATAGG					1020
188		TCTCTAGATA					1020
189 190		TTGTGGTTAA	•				1140
191		TCTGGTGGAG					1200
191		AACCTCTGGA					1260
193		GAGGCTGGAG					1320
194		TGTAAAGGGT					1380
195		GAGCCGTCTG					1440
196		GGCCTGGTTT					1500
197		GGGCCCATCG					1560
198		CCTGGGCTGC					1620
199		CGCCCTGACC					1680
200		CCTCAGCAGC					1740
201		CGTGAATCAC					1800
202		GGGAGGGAGG					1860
203						CCTCTTCACC	1.920
204		TGCCCGCCCC					1980
205		GGCACAGGCT					2040
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206	GCTGGGCTCA	GACCTGCCAA	GAGCCATATC	CGGGAGGACC	CTGCCCCTGA	CCTAAGCCCA	2100
207	CCCCAAAGGC	CAAACTCTCC	ACTCCCTCAG	CTCGGACACC	TTCTCTCCTC	CCAGATTCCA	2160
208	GTAACTCCCA	ATCTTCTCTC	TGCAGAGCCC	AAATCTTGTG	ACAAAACTCA	CACATGCCCA	2220
209	CCGTGCCCAG	GTAAGCCAGC	CCAGGCCTCG	CCCTCCAGCT	CAAGGCGGGA	CAGGTGCCCT	2280
210	AGAGTAGCCT	GCATCCAGGG	ACAGGCCCCA	GCCGGGTGCT	GACACGTCCA	CCTCCATCTC	2340
211	TTCCTCAGCA	CCTGAACTCC	TGGGGGGACC	GTCAGTCTTC	CTCTTCCCCC	CAAAACCCAA	2400
212			GGACCCCTGA				2460
213	CGAAGACCCT	GAGGTCAAGT	TCAACTGGTA	CGTGGACGGC	GTGGAGGTGC	ATAATGCCAA	2520
214			AGTACAACAG				2580
215	CCTGCACCAG	GACTGGCTGA	ATGGCAAGGA	GTACAAGTGC	AAGGTCTCCA	ACAAAGCCCT	2640
216			CCATCTCCAA				2700
217	GCCACATGGA	CAGAGGCCGG	CTCGGCCCAC	CCTCTGCCCT	GAGAGTGACC	GCTGTACCAA	2760
218	CCTCTGTCCC	TACAGGGCAG	CCCCGAGAAC	CACAGGTGTA	CACCCTGCCC	CCATCCCGGG	2820
219	•		GTCAGCCTGA				2880
220			AGCAATGGGC				2940
221			TCCTTCTTCC				3000
222			TTCTCATGCT				3060
223			CTGTCTCCGG				3120
224			CGCACGAGGA				3180
225			TAAAGCACCC				3240
226			GGCCGAGTCT				3300
227			TGGCCCAGGC				3360
228			CTCGGCAGGG				3420
229			GGGCCACGGG				3480
			GACTGTCCTG				3540
230			CCTAGTCCAT				3600
231			CCTGGCTGCC				3660
232							3720
233			ACTCTCGGGC				3780
234			GTTCAACAAA				
235			GCCTCACACA		•		3840
236			TCGCACACGT				3900
237			CCCACGAGCC				3960
238			TCTCACAAGG				4020
239			TCCCTGGCCC				4080
240			TGTGCCTTCT				4140
241			GGAAGGTGCC				4200
242			GAGTAGGTGT				4260
243			GGAAGACAAT				4320
244			AACCAGCTGG				4380
245			GGGTGTGGTG				4440
246			TTTCGCTTTC				4500
247			AAGCATGCAT				4560
248			CCTAACTCCG				4620
249			TGCAGAGGCC				4680
250			TGGAGGCCTA				4740
251			TTGACGGCAA				4800
252			ACCATTGAAC				4860
253			ACCCTGGCCT				4920
254			AGTGGAAGGT				4980
255			GAAGAATCGA				5040
256			ACCACGAGGA				5100 -
257			ACCGGAATTG				5160
258	GGAGGCAGTT	CTGTTTACCA	GGAAGCCATG	AATCAACCAG	GCCACCTTAG	ACTCTTTGTG	5220

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